

SEQUENCE LISTING

<110> Lacour, Thierry
 Rether, Jan
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 Schaefer, Wilhelm
 Maier, Frank
 Malz, Sascha

<120> Plasmid vectors for transformation of filamentous fungi

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<140> US 10/519,210

<141> 2004-12-23

<150> PCT/EP2003/007028

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<150> EP 02015067.8

<151> 2002-07-05

<150> EP 03008444.6

<151> 2003-04-11

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Glu Ile Gly Leu Gly	Leu Asp Val Leu Ser Asp Asp Glu Leu Asp Phe	
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Ala Asp His Gly Val Asp Ser Leu Leu Ser Leu Thr Ile Thr Gly Arg		
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Met Arg Glu Glu Leu Gly Leu Asp Val Glu Ser Thr Ala Phe Met Asn		
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Cys Pro Thr Leu Gly Ser Phe Lys Leu Phe Leu Gly Leu Val Asp Gln		
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Asp Asn Lys Gly Ser Ser Gly Ser Asp Gly Ser Gly Arg Ser Ser Pro		
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Ala Pro Gly Thr Glu Ser Gly Ala Thr Thr Pro Pro Met Ser Glu Glu		
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Ser Ser Thr Leu Leu Gln Gly Ser Pro Ser Lys Ala Arg Ser Thr Leu		
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Phe Leu Leu Pro Asp Gly Ser Gly Ser Ala Thr Ser Tyr Ala Ser Leu		
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Pro Pro Ile Ser Pro Asp Gly Asp Val Ala Val Tyr Gly Leu Asn Cys		
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Leu Thr Glu Leu Tyr Val Asn Glu Ile Leu Arg Arg Lys Pro Gln Gly		
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cct tac aat ttg gga gga tgg tca gcc ggt ggc att tgc gct tat gaa	5664	
Pro Tyr Asn Leu Gly Gly Trp Ser Ala Gly Gly Ile Cys Ala Tyr Glu		
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gct gcc ctg atc ctc acc aga gca gga cac caa gtc gat cgc ctt atc	5712	
Ala Ala Leu Ile Leu Thr Arg Ala Gly His Gln Val Asp Arg Leu Ile		
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Leu Ile Asp Ser Pro Asn Pro Val Gly Leu Glu Lys Leu Pro Pro Arg		

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Leu Tyr Asp Phe Leu Asn Ser Gln Asn Val Phe Gly Ser Asp Asn Pro				
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cac agc act gct gga aca agc gtc aaa gct cca gaa tgg ctt ctt gca				5856
His Ser Thr Ala Gly Thr Ser Val Lys Ala Pro Glu Trp Leu Leu Ala				
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cat ttc ctg gcc ttc att gac gct ctg gat gct tat gtc gca gtg cct				5904
His Phe Leu Ala Phe Ile Asp Ala Leu Asp Ala Tyr Val Ala Val Pro				
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tgg gac tct ggt cta gtc ggt cta gca tca ccg ctc cct gca ccg ccg				5952
Trp Asp Ser Gly Leu Val Gly Leu Ala Ser Pro Leu Pro Ala Pro Pro				
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Gln Thr Tyr Met Leu Trp Ala Glu Asp Gly Val Cys Lys Asp Ser Asp				
	1985	1990	2000	
agt gct cgt ccc gag tac cgt gac gat gac cca cgc gag atg aga tgg				6048
Ser Ala Arg Pro Glu Tyr Arg Asp Asp Asp Pro Arg Glu Met Arg Trp				
	2005	2010	2015	
ctg ttg gag aac aga aca aac ttt ggt ccg aat ggt tgg gag gcg cta				6096
Leu Leu Glu Asn Arg Thr Asn Phe Gly Pro Asn Gly Trp Glu Ala Leu				
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Leu Gly Gly Lys Glu Gly Leu Phe Met Asp Arg Ile Ala Glu Ala Asn				
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His Phe Ser Met Leu Lys Arg Gly Arg Asn Ala Glu Tyr Val Ser Ala				
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 1940 1945 1950

His Phe Leu Ala Phe Ile Asp Ala Leu Asp Ala Tyr Val Ala Val Pro
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Phe	Leu	Glu	Arg	Ala	Gly	Glu	Ala	Val	Arg	Phe	Glu	Asn	Gln	Asn	Arg	35	40	45	
Ser	His	Pro	Ser	Lys	Ala	Val	Pro	Asn	Phe	Ser	Thr	Ile	Gln	Glu	Leu	50	55	60	
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His	Ala	Ser	His	Xaa	His	Ser	Gln	Ser	Asp	Leu	Asp	Lys	Ile	Leu	Arg	245	250	255	
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 595 600 605
 Ile Met Lys Arg Leu Asp Asp Ala Leu Ala Asp Arg Asp Pro Val Leu
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 Ile Thr His Pro Cys Ala Glu Asn Gln Ala Phe Leu Phe Asp Lys Val
 645 650 655
 Leu Lys Glu Cys Asn Val His Cys Asn Asp Val Asn Tyr Val Glu Met
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 His Gly Thr Gly Thr Gln Ala Gly Asp Gly Ile Glu Met Glu Ser Val
 675 680 685
 Ser Ser Val Phe Ala Pro Arg Gln Pro Arg Arg Arg Pro Asp Gln Pro
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 Ser Gly Val Ser Ala Leu Ile Lys Val Leu Leu Met Leu Gln Lys Asn
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 Glu Val Pro Thr Glu Pro Ser Ser Asp Pro Arg Ser Thr His Val Val
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 Thr Xaa Ser Ala Lys Ser Leu Ala Ala Phe Lys Arg Thr Leu Ala Lys
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 850 855 860
 Phe Pro Val Gln Ser Ile Ser Gln Leu Gln Ala Ser Leu Arg Ala Ile
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Gln Asp Gln Thr His Asn Pro Ile Pro Leu Ala Ser Pro Gln Ile Ala
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 Glu Ile Ala Leu Arg Gln Gly Leu Pro Ser Ile Met Pro Leu Ile Asp
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 945 950 955 960
 Met Cys Cys Ile Gln Met Ala Leu Thr His Leu Trp Ser Thr Trp Gly
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Gln Pro Pro Ser Ala Glu Gly Gln Asp Met Ile Glu Thr Ile Arg Val
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 1925 1930 1935
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 1955 1960 1965
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 1985 1990 1995 2000
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 2005 2010 2015
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Thr Asp Gly Val Cys Gly Lys Pro Gly Asp Pro Arg Pro Pro Pro Gln
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Leu Gln Ser Met Asn Thr Val Asp His Lys Leu Ala Arg Thr Ala Asp
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```

```

Leu Arg Gln Met Val Gln Lys Tyr Val Asp Gly Lys Leu Thr Pro Ala
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Phe Arg Thr Ala Leu Val Cys Leu Cys Gln Leu Gly Cys Phe Ile Arg
      85             90            95

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Glu Tyr Glu Glu Ser Gly Asn Met Tyr Pro Gln Pro Ser Asp Ser Tyr
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Val Leu Gly Phe Cys Met Gly Ser Leu Ala Ala Val Ala Val Ser Cys
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Ser Arg Ser Leu Ser Glu Leu Leu Pro Ile Ala Val Gln Thr Val Leu
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 Cys Ala Met Pro Gln Met Ala Gln His Arg Thr Ala Pro Ile Pro Ile
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 625 630 635 640
 Ala Met Ser Glu Ser Met Thr Arg Pro His Val Gly Ala Gln Ile Asp
 645 650 655
 Asn Met Thr Ala Ala Leu Asn Thr Thr Gly Leu His Pro Asn Asp Phe
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 Ser Tyr Ile Glu Met His Gly Thr Gly Thr Gln Val Gly Asp Ala Val
 675 680 685
 Glu Met Glu Ser Val Leu Ser Val Phe Ala Pro Ser Glu Thr Ala Arg
 690 695 700
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 Ala His Pro Ala His Val Asp Ala Ile Thr Gln Val Ala Gly Phe Ala
 1540 1545 1550
 Met Asn Ala Asn Asp Asn Val Asp Ile Glu Lys Gln Val Tyr Val Asn
 1555 1560 1565
 His Gly Trp Asp Ser Phe Gln Ile Tyr Gln Pro Leu Asp Asn Ser Lys
 1570 1575 1580
 Ser Tyr Gln Val Tyr Thr Lys Met Gly Gln Ala Lys Glu Asn Asp Leu
 1585 1590 1595 1600
 Val His Gly Asp Val Val Val Leu Asp Gly Glu Gln Ile Val Ala Phe
 1605 1610 1615
 Phe Arg Gly Leu Thr Leu Arg Ser Val Pro Arg Gly Ala Leu Arg Val
 1620 1625 1630
 Val Leu Gln Thr Thr Val Lys Lys Ala Asp Arg Gln Leu Gly Phe Lys
 1635 1640 1645
 Thr Met Pro Ser Pro Pro Pro Pro Thr Thr Thr Met Pro Ile Ser Pro
 1650 1655 1660
 Tyr Lys Pro Ala Asn Thr Gln Val Ser Ser Gln Ala Ile Pro Ala Glu
 1665 1670 1675 1680
 Ala Thr His Ser His Thr Pro Pro Gln Pro Lys His Ser Pro Val Pro
 1685 1690 1695

Glu Thr Ala Gly Ser Ala Pro Ala Ala Lys Gly Val Gly Val Ser Asn
 1700 1705 1710
 Glu Lys Leu Asp Ala Val Met Arg Val Val Ser Glu Glu Ser Gly Ile
 1715 1720 1725
 Ala Leu Glu Glu Leu Thr Asp Asp Ser Asn Phe Ala Asp Met Gly Ile
 1730 1735 1740
 Asp Ser Leu Ser Ser Met Val Ile Gly Ser Arg Phe Arg Glu Asp Leu
 1745 1750 1755 1760
 Gly Leu Asp Leu Gly Pro Glu Phe Ser Leu Phe Ile Asp Cys Thr Thr
 1765 1770 1775
 Val Arg Ala Leu Lys Asp Phe Met Leu Gly Ser Gly Asp Ala Gly Ser
 1780 1785 1790
 Gly Ser Asn Val Glu Asp Pro Pro Pro Ser Ala Thr Pro Gly Ile Asn
 1795 1800 1805
 Pro Glu Thr Asp Trp Ser Ser Ser Ala Ser Asp Ser Ile Phe Ala Ser
 1810 1815 1820
 Glu Asp His Gly His Ser Ser Glu Ser Gly Ala Asp Thr Gly Ser Pro
 1825 1830 1835 1840
 Pro Ala Leu Asp Leu Lys Pro Tyr Cys Arg Pro Ser Thr Ser Val Val
 1845 1850 1855
 Leu Gln Gly Leu Pro Met Val Ala Arg Lys Thr Leu Phe Met Leu Pro
 1860 1865 1870
 Asp Gly Gly Gly Ser Ala Phe Ser Tyr Ala Ser Leu Pro Arg Leu Lys
 1875 1880 1885
 Ser Asp Thr Ala Val Val Gly Leu Asn Cys Pro Tyr Ala Arg Asp Pro
 1890 1895 1900
 Glu Asn Met Asn Cys Thr His Gly Ala Met Ile Glu Ser Phe Cys Asn
 1905 1910 1915 1920
 Glu Ile Arg Arg Arg Gln Pro Arg Gly Pro Tyr His Leu Gly Gly Trp
 1925 1930 1935
 Ser Ser Gly Gly Ala Phe Ala Tyr Val Val Ala Glu Ala Leu Val Asn
 1940 1945 1950
 Gln Gly Glu Glu Val His Ser Leu Ile Ile Ile Asp Ala Pro Ile Pro
 1955 1960 1965
 Gln Ala Met Glu Gln Leu Pro Arg Ala Phe Tyr Glu His Cys Asn Ser
 1970 1975 1980
 Ile Gly Leu Phe Ala Thr Gln Pro Gly Ala Ser Pro Asp Gly Ser Thr
 1985 1990 1995 2000

Val Ala Leu Arg Leu Gly Leu Cys Val Tyr Arg Val Arg Lys Leu Phe

145 150 155 160
 Gly Gln Asp Gln Ala Ala Pro Leu Ser Trp Ser Ala Leu Val Ser Gly
 165 170 175
 Leu Ser Glu Ser Glu Gly Thr Ser Leu Ile Asp Lys Phe Thr Arg Arg
 180 185 190
 Asn Val Ile Pro Pro Ser Ser Arg Pro Tyr Ile Ser Ala Val Cys Ala
 195 200 205
 Asn Thr Leu Thr Ile Ser Gly Pro Pro Val Val Leu Asn Gln Phe Leu
 210 215 220
 Asp Thr Phe Ile Ser Gly Lys Asn Lys Ala Val Met Val Pro Ile His
 225 230 235 240
 Gly Pro Phe His Ala Ser His Leu Tyr Glu Lys Arg Asp Val Glu Trp
 245 250 255
 Ile Leu Lys Ser Cys Asn Val Glu Thr Ile Arg Asn His Lys Pro Arg
 260 265 270
 Ile Pro Val Leu Ser Ser Asn Thr Gly Glu Leu Ile Val Val Glu Asn
 275 280 285
 Met Glu Gly Phe Leu Lys Ile Ala Leu Glu Glu Ile Leu Leu Arg Gln
 290 295 300
 Met Ser Trp Asp Lys Val Thr Asp Ser Cys Ile Ser Ile Leu Lys Ser
 305 310 315 320
 Val Gly Asp Asn Lys Pro Lys Lys Leu Leu Pro Ile Ser Ser Thr Ala
 325 330 335
 Thr Gln Ser Leu Phe Asn Ser Leu Lys Lys Ser Asn Leu Val Asn Ile
 340 345 350
 Glu Val Asp Gly Gly Ile Ser Asp Phe Ala Ala Glu Thr Gln Leu Val
 355 360 365
 Asn Gln Thr Gly Arg Ala Glu Leu Ser Lys Ile Ala Ile Ile Gly Met
 370 375 380
 Ser Gly Arg Phe Pro Glu Ala Asp Ser Pro Gln Asp Phe Trp Asn Leu
 385 390 395 400
 Leu Tyr Lys Gly Leu Asp Val His Arg Lys Val Pro Glu Asp Arg Trp
 405 410 415
 Asp Ala Asp Ala His Val Asp Leu Thr Gly Thr Ala Thr Asn Thr Ser
 420 425 430
 Lys Val Pro Tyr Gly Cys Trp Ile Arg Glu Pro Gly Leu Phe Asp Pro
 435 440 445
 Arg Phe Phe Asn Met Ser Pro Arg Glu Ala Leu Gln Ala Asp Pro Ala

450		455		460
Gln Arg Leu Ala Leu Leu Thr Ala Tyr Glu Ala Leu Glu Gly Ala Gly				
465		470		480
Phe Val Pro Asp Ser Thr Pro Ser Thr Gln Arg Asp Arg Val Gly Ile				
	485		490	495
Phe Tyr Gly Met Thr Ser Asp Asp Tyr Arg Glu Val Asn Ser Gly Gln				
	500		505	510
Asp Ile Asp Thr Tyr Phe Ile Pro Gly Gly Asn Arg Ala Phe Thr Pro				
	515		520	525
Gly Arg Ile Asn Tyr Tyr Phe Lys Phe Ser Gly Pro Ser Val Ser Val				
	530		535	540
Asp Thr Ala Cys Ser Ser Ser Leu Ala Ala Ile His Leu Ala Cys Asn				
	545		550	560
Ser Ile Trp Arg Asn Asp Cys Asp Thr Ala Ile Thr Gly Gly Val Asn				
	565		570	575
Ile Leu Thr Asn Pro Asp Asn His Ala Gly Leu Asp Arg Gly His Phe				
	580		585	590
Leu Ser Arg Thr Gly Asn Cys Asn Thr Phe Asp Asp Gly Ala Asp Gly				
	595		600	605
Tyr Cys Arg Ala Asp Gly Val Gly Thr Val Val Leu Lys Arg Leu Glu				
	610		615	620
Asp Ala Leu Ala Asp Asn Asp Pro Ile Leu Gly Val Ile Asn Gly Ala				
	625		630	640
Tyr Thr Asn His Ser Ala Glu Ala Val Ser Ile Thr Arg Pro His Val				
	645		650	655
Gly Ala Gln Ala Phe Ile Phe Lys Lys Leu Leu Asn Glu Ala Asn Val				
	660		665	670
Asp Pro Lys Asn Ile Ser Tyr Ile Glu Met His Gly Thr Gly Thr Gln				
	675		680	685
Ala Gly Asp Ala Val Glu Met Gln Ser Val Leu Asp Val Phe Ala Pro				
	690		695	700
Asp His Arg Arg Gly Pro Gly Gln Ser Leu His Leu Gly Ser Ala Lys				
	705		710	715
Ser Asn Ile Gly His Gly Glu Ser Ala Ser Gly Val Thr Ser Leu Val				
	725		730	735
Lys Val Leu Leu Met Met Lys Glu Asn Met Ile Pro Pro His Cys Gly				
	740		745	750
Ile Lys Thr Lys Ile Asn His Asn Phe Pro Thr Asp Leu Ala Gln Arg				

755	760	765
Asn Val His Ile Ala Leu Gln Pro Thr Ala Trp Asn Arg Pro Ser Phe 770 775 780		
Gly Lys Arg Gln Ile Phe Leu Asn Asn Phe Ser Ala Ala Gly Gly Asn 785 790 795 800		
Thr Ala Leu Leu Leu Glu Asp Gly Pro Val Ser Asp Pro Glu Gly Glu 805 810 815		
Asp Lys Arg Arg Thr His Val Ile Thr Leu Ser Ala Arg Ser Gln Thr 820 825 830		
Ala Leu Gln Asn Asn Ile Asp Ala Leu Cys Gln Tyr Ile Ser Glu Gln 835 840 845		
Glu Lys Thr Phe Gly Val Lys Asp Ser Asn Ala Leu Pro Ser Leu Ala 850 855 860		
Tyr Thr Thr Thr Ala Arg Arg Ile His His Pro Phe Arg Val Thr Ala 865 870 875 880		
Ile Gly Ser Ser Phe Gln Glu Met Arg Asp Ser Leu Ile Ala Ser Ser 885 890 895		
Arg Lys Glu Phe Val Ala Val Pro Ala Lys Thr Pro Gly Ile Gly Phe 900 905 910		
Leu Phe Thr Gly Gln Gly Ala Gln Tyr Ala Ala Met Gly Lys Gln Leu 915 920 925		
Tyr Glu Asp Cys Ser His Phe Arg Ser Ala Ile Glu His Leu Asp Cys 930 935 940		
Ile Ser Gln Gly Gln Asp Leu Pro Ser Ile Leu Pro Leu Val Asp Gly 945 950 955 960		
Ser Leu Pro Leu Ser Glu Leu Ser Pro Val Val Val Gln Leu Gly Thr 965 970 975		
Thr Cys Val Gln Met Ala Leu Ser Ser Phe Trp Ala Ser Leu Gly Ile 980 985 990		
Thr Pro Ser Phe Val Leu Gly His Ser Leu Gly Asp Phe Ala Ala Met 995 1000 1005		
Asn Ala Ala Gly Val Leu Ser Thr Ser Asp Thr Ile Tyr Ala Cys Gly 1010 1015 1020		
Arg Arg Ala Gln Leu Leu Thr Glu Arg Cys Gln Pro Gly Thr His Ala 1025 1030 1035 1040		
Met Leu Ala Ile Lys Ala Pro Leu Val Glu Val Lys Gln Leu Leu Asn 1045 1050 1055		
Glu Lys Val His Asp Met Ala Cys Ile Asn Ser Pro Ser Glu Thr Val		

1060	1065	1070
Ile Ser Gly Pro Lys Ser Ser Ile Asp Glu Leu Ser Arg Ala Cys Ser 1075	1080	1085
Glu Lys Gly Leu Lys Ser Thr Ile Leu Thr Val Pro Tyr Ala Phe His 1090	1095	1100
Ser Ala Gln Val Glu Pro Ile Leu Glu Asp Leu Glu Lys Ala Leu Gln 1105	1110	1115 1120
Gly Ile Thr Phe Asn Lys Pro Ser Val Pro Phe Val Ser Ala Leu Leu 1125	1130	1135
Gly Glu Val Ile Thr Glu Ala Gly Ser Asn Ile Leu Asn Ala Glu Tyr 1140	1145	1150
Leu Val Arg His Cys Arg Glu Thr Val Asn Phe Leu Ser Ala Phe Glu 1155	1160	1165
Ala Val Arg Asn Ala Lys Leu Gly Gly Asp Gln Thr Leu Trp Leu Glu 1170	1175	1180
Val Gly Pro His Thr Val Cys Ser Gly Met Val Lys Ala Thr Leu Gly 1185	1190	1195 1200
Pro Gln Thr Thr Thr Met Ala Ser Leu Arg Arg Asp Glu Asp Thr Trp 1205	1210	1215
Lys Val Leu Ser Asn Ser Leu Ser Ser Leu Tyr Leu Ala Gly Val Asp 1220	1225	1230
Ile Asn Trp Lys Gln Tyr His Gln Asp Phe Ser Ser Ser His Arg Val 1235	1240	1245
Leu Pro Leu Pro Thr Tyr Lys Trp Asp Leu Lys Asn Tyr Trp Ile Pro 1250	1255	1260
Tyr Arg Asn Asn Phe Cys Leu Thr Lys Gly Ser Ser Met Ser Ala Ala 1265	1270	1275 1280
Ser Ala Ser Leu Gln Pro Thr Phe Leu Thr Thr Ser Ala Gln Arg Val 1285	1290	1295
Val Glu Ser Arg Asp Asp Gly Leu Thr Ala Thr Val Val Val His Asn 1300	1305	1310
Asp Ile Ala Asp Pro Asp Leu Asn Arg Val Ile Gln Gly His Lys Val 1315	1320	1325
Asn Gly Ala Ala Leu Cys Pro Ser Ser Leu Tyr Ala Asp Ser Ala Gln 1330	1335	1340
Thr Leu Ala Glu Tyr Leu Ile Glu Lys Tyr Lys Pro Glu Leu Lys Gly 1345	1350	1355 1360
Ser Gly Leu Asp Val Cys Asn Val Thr Val Pro Lys Pro Leu Ile Ala		

1365	1370	1375
Lys Thr Gly Lys Glu Gln Phe Arg Ile Ser Ala Thr Ala Asn Trp Val 1380	1385	1390
Asp Lys His Val Ser Val Gln Val Phe Ser Val Thr Ala Glu Gly Lys 1395	1400	1405
Lys Leu Ile Asp His Ala His Cys Glu Val Lys Leu Phe Asp Cys Met 1410	1415	1420
Ala Ala Asp Leu Glu Trp Lys Arg Gly Ser Tyr Leu Val Lys Arg Ser 1425	1430	1435
Ile Glu Leu Leu Glu Asn Ser Ala Val Lys Gly Asp Ala His Arg Leu 1445	1450	1455
Arg Arg Gly Met Val Tyr Lys Leu Phe Ser Ala Leu Val Asp Tyr Asp 1460	1465	1470
Glu Asn Tyr Gln Ser Ile Arg Glu Val Ile Leu Asp Ser Glu His His 1475	1480	1485
Glu Ala Thr Ala Leu Val Lys Phe Gln Ala Pro Gln Ala Asn Phe His 1490	1495	1500
Arg Asn Pro Tyr Trp Ile Asp Ser Phe Gly His Leu Ser Gly Phe Ile 1505	1510	1515
Met Asn Ala Ser Asp Gly Thr Asp Ser Lys Ser Gln Val Phe Val Asn 1525	1530	1535
His Gly Trp Asp Ser Met Arg Cys Leu Lys Lys Phe Ser Ala Asp Val 1540	1545	1550
Thr Tyr Arg Thr Tyr Val Arg Met Gln Pro Trp Arg Asp Ser Ile Trp 1555	1560	1565
Ala Gly Asn Val Tyr Ile Phe Glu Gly Asp Asp Ile Ile Ala Val Phe 1570	1575	1580
Gly Gly Val Lys Phe Gln Ala Leu Ser Arg Lys Ile Leu Asp Ile Ala 1585	1590	1595
Leu Pro Pro Ala Gly Leu Ser Lys Ala Gln Thr Ser Pro Ile Gln Ser 1605	1610	1615
Ser Ala Pro Gln Lys Pro Ile Glu Thr Ala Lys Pro Thr Ser Arg Pro 1620	1625	1630
Ala Pro Pro Val Thr Met Lys Ser Phe Val Lys Lys Ser Ala Gly Pro 1635	1640	1645
Ser Val Val Val Arg Ala Leu Asn Ile Leu Ala Ser Glu Val Gly Leu 1650	1655	1660
Ser Glu Ser Asp Met Ser Asp Asp Leu Val Phe Ala Asp Tyr Gly Val		

1665	1670	1675	1680
Asp Ser Leu Leu Ser Leu Thr Val Thr Gly Lys Tyr Arg Glu Glu Leu			
1685	1690	1695	
Asn Leu Asp Met Asp Ser Ser Val Phe Ile Glu His Pro Thr Val Gly			
1700	1705	1710	
Asp Phe Lys Arg Phe Val Thr Gln Leu Ser Pro Ser Val Ala Ser Asp			
1715	1720	1725	
Ser Ser Ser Thr Asp Arg Glu Ser Glu Tyr Ser Phe Asn Gly Asp Ser			
1730	1735	1740	
Cys Ser Gly Leu Ser Ser Pro Ala Ser Pro Gly Thr Val Ser Pro Pro			
1745	1750	1755	1760
Asn Glu Lys Val Ile Gln Ile His Glu Asn Gly Thr Met Lys Glu Ile			
1765	1770	1775	
Arg Ala Ile Ile Ala Asp Glu Ile Gly Val Ser Ala Asp Glu Ile Lys			
1780	1785	1790	
Ser Asp Glu Asn Leu Asn Glu Leu Gly Met Asp Ser Leu Leu Ser Leu			
1795	1800	1805	
Thr Val Leu Gly Lys Ile Arg Glu Ser Leu Asp Met Asp Leu Pro Gly			
1810	1815	1820	
Glu Phe Phe Ile Glu Asn Gln Thr Leu Asp Gln Ile Glu Thr Ala Leu			
1825	1830	1835	1840
Asp Leu Lys Pro Lys Ala Val Pro Thr Ala Val Pro Gln Ser Gln Pro			
1845	1850	1855	
Ile Thr Leu Pro Gln Ser Gln Ser Thr Lys Gln Leu Ser Thr Arg Pro			
1860	1865	1870	
Thr Ser Ser Ser Asp Asn His Pro Pro Ala Thr Ser Ile Leu Leu Gln			
1875	1880	1885	
Gly Asn Pro Arg Thr Ala Ser Lys Thr Leu Phe Leu Phe Pro Asp Gly			
1890	1895	1900	
Ser Gly Ser Ala Thr Ser Tyr Ala Thr Ile Pro Gly Val Ser Pro Asn			
1905	1910	1915	1920
Val Ala Val Tyr Gly Leu Asn Cys Pro Tyr Met Lys Ala Pro Glu Lys			
1925	1930	1935	
Leu Thr Cys Ser Leu Asp Ser Leu Thr Thr Pro Tyr Leu Ala Glu Ile			
1940	1945	1950	
Arg Arg Arg Gln Pro Thr Gly Pro Tyr Asn Leu Gly Gly Trp Ser Gln			
1955	1960	1965	
Ala Gly Ser Ala His Thr Thr Arg His Ala Ser Ser Tyr Cys Ser Arg			

1970

1975

1980

Ala Lys
1985

<210> 14
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
atgaagcttg gggtttgagg gccaatggaa cgaaactagt gtaccacttg acc 53

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
gacagatctg gcgccattcg ccattcag 28

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ggaatcggtc aatacactac 20

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
tgtagatctc tattcctttg ccctcggacg agt 33

<210> 18
<211> 35
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 18

ggccgccacg gatattttgg ccaaagaatt cctgg

35

<210> 19

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

cgggtgcctat agaaccggtt tcttaaggac cgcgc

35

<210> 20

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

gayccmgtty ttyaayatg

19

<210> 21

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21

gtccgtccrt gcatytc

17

<210> 22

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 22

ataagaatgc ggccgcaatg gccctcgaaa cagc

34

<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
aatggcgcg ccgccccag aatgacacc 29

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
tgccacctgt agtctgcaat cag 23

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
tgactaacc tgacaacttc gctg 24

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
ccaggatccg actgctcag 19

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27

ctacatcgag atgcacggca c

21

<210> 28
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> n is a, c, g, t, unknown, or other

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> n is a, c, g, t, unknown, or other

<400> 28
 ngtcgaswga nawgaa

16

<210> 29
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> n is a, c, g, t, unknown, or other

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> n is a, c, g, t, unknown, or other

<400> 29
 gtncgaswca nawgtt

16

<210> 30
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> misc_feature

<222> (5)..(5)
 <223> n is a, c, g, t, unknown, or other

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> n is a, c, g, t, unknown, or other

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> n is a, c, g, t, unknown, or other

<400> 30
 wgtgnagwan canaga

16

<210> 31
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
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 <222> (1)..(1)
 <223> n is a, c, g, t, unknown, or other

<400> 31
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15

<210> 32
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> n is a, c, g, t, unknown, or other

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> n is a, c, g, t, unknown, or other

<400> 32
 tgwnagwan casaga

16

<210> 33

<211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> n is a, c, g, t, unknown, or other

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> n is a, c, g, t, unknown, or other

<400> 33
 agwgnagwan cawagg

16

<210> 34
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
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 <222> (7)..(7)
 <223> n is a, c, g, t, unknown, or other

<400> 34
 cawcgngaa sgaa

14

<210> 35
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> misc_feature
 <222> (7)..(7)
 <223> n is a, c, g, t, unknown, or other

<400> 35
 tcstcgnact wgga

14

<210> 36
 <211> 23

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 36
 ttgttactgg agaggtaatg aag 23

<210> 37
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 37
 tgagacagat ctcgcgagcc ctc 23

<210> 38
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 38
 atgtctccaa aggaagctga gc 22

<210> 39
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 39
 tcgagtgatg gatactgctt cg 22

<210> 40
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 40
 cggctacact agaaggacag tatttggtta 29

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
gtcaggcaac tatggatgaa cgaaatagac 30

<210> 42
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
acccatctca taaataacgt catgc 25

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 43
caactctatc agagcttggt tga 23

<210> 44
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 44
cccgaattca tgagctttgt tcaaataagg 30

<210> 45
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
ttattctaga ttttccatgg gaatggatac agtcttacg 39

<210> 46
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 46
cgccaccatg gtgagcaagg gcgaggagct gtt 33

<210> 47
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
tatgatctag agtcgcggcc gctttacttg tacagctcg 39

<210> 48
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
gcttctaatac cgtactagtg gatca 25

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
ctttgatctt ttctacgggg tctga 25